

### SUMMARY OF SEQUENCES

SEQ ID NO: 1 is the N-terminal amino acid sequence for the YKL-40 protein.

SEQ ID NO: 2 is an internal amino acid sequence for the YKL-40 protein ("YKL-40 Peptide A").

5 SEQ ID NO: 3 is another internal amino acid sequence for the YKL-40 protein ("YKL-40 Peptide B").

SEQ ID NO: 4 is the cDNA nucleotide sequence for the coding region of the gene for YKL-40. The initiation codon for the mature, secreted protein begins at nucleotide 135.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

5 (ii) TITLE OF INVENTION: ASSAY FOR YKL-40 AS A MARKER FOR  
DEGRADATION OF MAMMALIAN CONNECTIVE TISSUE MATRICES

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
(B) STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
(C) CITY: LOS ANGELES  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
15 (F) ZIP: 90067

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
20 (D) SOFTWARE: Patent In Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT  
(B) FILING DATE: 08-JUL-1994  
(C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HOWELLS, STACY L.  
(B) REGISTRATION NUMBER: 34,842  
(C) REFERENCE/DOCKET NUMBER: FD 3665

(ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: 619/455-5100  
(B) TELEFAX: 619/455-5110

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 25 amino acids  
(B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: YKL-40 N-TERMINAL SEQUENCE

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser Gln Tyr Arg Glu Gly  
1 5 10 15

Asp Gly Ser Xaa Phe Pro Asp Ala Leu  
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: YKL-40 INTERNAL PEPTIDE A

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser  
1 5 10 15

Val Gly Gly

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: YKL-40 INTERNAL PEPTIDE B

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Leu Arg Leu Gly Ala Pro Ala  
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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: YKL-40

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 135..1681

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CTAGGTAGCT GGCACCAGGA GCCGTGGGCA AGGGAAGAGG CCACACCCTG CCCTGCTCTG 60  
 CTGCAGCCAG AATGGGTGTG AAGGCGTCTC AAACAGGCTT TGTGGTCCTG GTGCTGCTCC 120  
 AGTGCTGCTC TGCATACAAA CTGGTCTGCT ACTACACCAG CTGGTCCCAG TACCGGGAAG 180  
 GCGATGGGAG CTGCTTCCCA GATGCCCTTG ACCGCTTCCT GTGTACCCAC ATCATCTACA 240  
 5 GCTTTGCCAA TATAAGCAAC GATCACATCG ACACCTGGGA GTGGAATGAT GTGACGCTCT 300  
 ACGGCATGCT CAACACACTC AACAAACAG AACCACCTT GAAGACTCTC TTGTCTGTCTG 360  
 GAGGATGGAA CTTTGGGTCT CAAAGATTTT CCAAGATAGC CTCCAACACC CAGAGTCGCC 420  
 GGACTTTCAT CAAGTCAGTA CCGCCATTTC TGCGCACCCA TGGCTTTGAT GGGCGTGACC 480  
 TTGCCTGGCT CTACCCTGGA CGGAGAGACA AACACCATTT TACCACCCTA ATCAAGGAAA 540  
 10 TGAAGGCCGA ATTTATAAAG GAAGCCCAGC CAGGGAAAAA GCAGCTCCTG CTCAGCGCAG 600  
 CACTGTCTGC GGGGAAGGTC ACCATTGACA GCAGCTATGA CATTGCGAAG ATATCCCAAC 660  
 ACCTGGATTT CATTAGCATC ATGACCTACG ATTTTCATGG CGCCTGGCGT GGGACCACAG 720  
 GCCATCACAG TCCCCTGTTC CGAGGTCAGG AGGATGCAAG TCCTGACAGA TTCAGCAACA 780  
 CTGACTATGC TGTGGGGTAC ATGTTGAGGC TGGGGGCTCC TGCCAGTAAG CTGGTGATGG 840  
 15 GCATCCCCAC CTTGCGGAGG AGCTTCACTC TGGCTTCTTC TGAGACTGGT GTTCCAGCGC 900  
 CAATCTCAGG ACCGGGAATT CCAGGCCGGT TCACCAAGGA GGCAGGGACC CTTGCCTACT 960  
 ATGAGATCTG TGACTTCCTC CGCGGAGCCA CAGTCCATAG AACCTCGGC CAGCAGGTCC 1020  
 CCTATGCCAC CAAGGGCAAC CAGTGGGTAG GATACGACGA CCAGGAAAGC GTCAAAAGCA 1080  
 AGGTGCAGTA CCTGAAGGAT AGGCAGCTGG CAGGCGCCAT GGTATGGGCC CTGGACCTGG 1140  
 20 ATGACTTCCA GGGCTCCTTC TGCGGCCAGG ATCTGCGCTT CCCTCTCACC AATGCCATCA 1200  
 AGGATGCACT CGCTGCAACG TAGCCCTCTG TTCTGCACAC AGCACGGGGG CCAAGGATGC 1260  
 CCCGTCCCCG TCTGGCTGGC CGGGAGCCTG ATCACCTGCC CTGCTGAGTC CCAGGCTGAG 1320  
 CCTCAGTCTC CCTCCCTTGG GGCCTATGCA GAGGTCCACA ACACACAGAT TTGAGCTCAG 1380

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CCCTGGTGGG CAGAGAGGTA CACACTTGTT GATGATTAAT GGAAATGTTT ACAGATCCCC 1440  
AAGCCTGGCA AGGGAATTC TTCAACTCCC TGCCCCCTAG CCCTCCTTAT CAAAGGACAC 1500  
CATTGTGGCA AGCTCTATCA CCAAGGAGCC AACATCCTA CAAGACACAG TGACCATACT 1560  
AATTATACCC CTGCAAAGC CACTTGAAA CCTTCACTTA GGAACGTAAT CGTGTCCCCT 1620  
5 ATCCTACTTC CCCTTCCTAA TTCCACAGCT GCTCAATAAA GTACAAGAGT TTAACAGTGT 1680  
G 1681

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